

1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library.
 BASE COUNT 182 a 203 c 216 g 138 t
 ORIGIN

Query Match 56.2%; Score 728; DB 10; Length 739;
 Best Local Similarity 99.9%; Pred. No. 1.4e-65;
 Matches 739; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 29 aggaagtctcgggaccagatcagagacatgttcgagcagggtaagtgggacgtgtttt 88
 Db 1 AGGAAGTCTCGGCGACAGATCAGGACATGTTCCGAGCAGGGTAAGTGGGACGTGTTT 60
 QY 89 ccgagaactctgtcgcgcagcgtgaagggcgcgcgccctcaacagagatcagagacc 148
 -- 61 CCGAGAAGTCTGCTGGCGACGTGAAGGGCGCGCGCCCTCAACGAGATCGAGAGCC 120
 -- 149 gccaccgcgaactgtcgtcgtgagagcgcgcacccgagcgtacacagagctcttctgc 208
 Db 121 GCCACCGCGAAGTCTGCGCTGGAGAGCCGATCCGCGAGCTACAGAGCTCTTCTTGC 180
 QY 209 agatggcggtgctggtgagaagcagccgacacccctgaaagcgtcatcgagctcaacgtac 268
 Db 181 AGATGGCGGTGCTGTTGAGAGCAGCGCCGACACCTGAGAGTCTGAGTCAACGTAC 240
 QY 269 aaagacggtcgtactacacccgagcagccgagcgcgagggcgcgagggcgcgagcgcg 328
 Db 241 AAAAGCGGTGCTGATACACCGCGCAGCGCAGGCGAGGCGGCGGCGGCGGCGGCGG 300
 QY 329 agagaagaacccctgcgcgacccctcgtcttctcgtctcctcgtcctcgtcctcgtcct 388
 Db 301 AGAGAAGAAGACCCCTGCGGACCCCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTG 360
 QY 389 ccgcccgcggcgccgacccgacccatcccgagacccatggagcgcgctgggagagcgtcacc 448
 Db 361 CCG 419
 QY 449 aagccggagcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 508
 Db 420 AAGCCGGAGCTGTGCGCTCAGGAGTGTGCCCAACCTTCCGGAACCTGAGTCACTTAT 479
 QY 509 aaagaagccaggttcaagaattcaaacacagcgtgctgctggaagatggttagttg 568
 Db 480 AAAAGAAACCCAGGTTCAAGATTGCAACACAGCCCTGCTGCTGCTGCTGCTGCTGCTG 539
 QY 569 ataccgtccgagtgattcttcagtaaaagatagattcccaaaagtgtgtcaatgtcattat 628
 Db 540 ATACCGTCCGATGATCTTTCAGTAAGATAGATTCCCAAAAGTTGTGCAATGTCATTAT 599
 QY 629 atgaacacctgactcttaccgtcttgagagagcgaagtaaggaactgaagttgtatct 688
 Db 600 ATGACACCTTGCCTTCTTACCGCTTTGACAGAGAGCCAAAGTAAGTAAGTGTATCT 659
 QY 689 gactgtagggtgaatgtctgagccctcctcctaataaagactcaaggaagtaagtaatt 748
 Db 660 GACTGTAGGTGAATGTCTGAGCGCTTCCCTCTTAATAAGACTCAAGGAGGAGTCAATT 719
 QY 749 gggcatctcgtataagaatt 768
 Db 720 GGSCATCTGCTATAGAAATG 739

RESULT 2
 B1519530/c
 LOCUS 911 bp mRNA linear EST 29-AUG-2001
 DEFINITION 603061815T1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5211074 3',
 mRNA sequence.
 ACCESSION B1519530
 VERSION B1519530.1 GI:15344322
 KEYWORDS EST.

SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 911)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cspbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM1529 row: n column: 03
 High quality sequence start: 3
 High quality sequence stop: 890.

FEATURES
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5211074"
 /clone_lib="NIH_MGC_118"
 /tissue_type="leukocyte"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
 (destroyed); RNA source leukocytes from anonymous pool of
 non-activated adult donors. Library is oligo-dT primed
 and directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb, insert size range
 1.2-3.3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 027. Note:
 this is a NIH_MGC Library."
 BASE COUNT 199 a 235 c 243 g 234 t
 ORIGIN

Query Match 50.9%; Score 658.6; DB 10; Length 911;
 Best Local Similarity 94.8%; Pred. No. 3.6e-62;
 Matches 854; Conservative 0; Mismatches 29; Indels 18; Gaps 16;
 QY 37 tcggggaccagatcgaggacatgtt--cgagcaggggtaagtgggacgtgttttc-cgag 93
 Db 900 TCGGGGACCAAGATCGAGACATGTTTCGAGCAAGGGTAAGTGAACGCTGTTTTCACGAG 841
 QY 94 aactt-gctggcagctgaaggcgcgcgccg-cctcaacgagatcgagaccgcc 151
 Db 840 AACTTCGCTTGGCGACGTTAAGGGCGCGCGCGCCCTCAACGAGATCGAGAGCCGCC 781
 QY 152 a-cgcgaactgtcgcctgagagcgcgcacccgagctacacgagctctcttgcag 210
 Db 780 ATCCGCGAAGTGTGCGCATGGATAGCGCATCGCGCAACGTACAGACGCTCTCTTGAG 721
 QY 211 atggtc-ggtgctggtgagaagca-ggcgcacacccctgaacgtcatcgagctcaacgtac 268
 Db 720 ATGCTGCTGCTGTTGGAGAGCATGGCGGACACCTTGAACGTCATCGAGTCAACGTAC 661
 QY 269 aaaag-acggtcgactacacccggc-caggccaagggcgaggt-gcggaagggcgtgcagt 325
 Db 660 AAAAGTACGCTGCTGAGAGAGCATGGCGGACAGGCGCAAGCGCAGGTAGCGGAAGCCGTGCAGT 601
 QY 326 acgaggagaagaacccctgctgcgaccctctgctcttctctcctgcctcgaagtagc 385
 Db 600 ACGAGGAGAGAACCCCTGCGGACCTCTGCTGCTCTCTGCTGCTCTCTGCTCAAGTAGC 541
 QY 386 aggcgggcccggcgccgacacccatccagacatggagcgcgctgggagagcgtca 445
 Db 540 AGGCGGCG 482

Db	426	CATCCGACGACTACACGAGCTTCTTTGAGATGGCGGTGCTGGTGAGAGCAGGCCGA	367
Qy	240	caccctgaacgtcatcgagctcaacgtcaaaaagacggttcgactacaccgagcga	299
Db	366	CACCCTACGCTCATCGAGCTCAACGTACAAAAGACGGTCGACTACACGCCAGGCCAA	307
Qy	300	ggcgagtgctgggaagcgctgcagtagcagaggaagaacccctgccgagccctctctg	359
Db	306	GGCGAGGTGCGGAAGCGCTGAGTACGAGGAGGAGAAACACTTCCCGGACCCCTCTGCTG	247
Qy	360	cttcgtgtccctgcctcaagtagcagcgccgcccggcgccacccgcatcccaagac	419
Db	246	CTTCTGCTGTCCCTGCTCAAGTAGCAGGCGCGCCCGCGCCACACCGCCATCCCGAC	187
Qy	420	catgagcgcgctgggaagcagctcacaaagccgggagctctgcctcgcaggagttgc	479
Db	186	CATGACGCGGCTGGGAGGACG-CACCAAAAGCGGAGGACTCTG-CTTGAGGAGGTTGC	129
Qy	480	cccaacccttcgggaactcagctctttagaaaagaacgcaggttcaagaattgcaaac	539
Db	128	CCCAACCTTTCGGAACCTCAGTCTTTAGAAAAGAAACGCCAGGTTCAAGAAATTCGCAAC	69
Qy	540	cagcctgtgttgaaagatggttagtgatcacgtccgtagctattcttcagtaaatag	599
Db	68	CAGCCTGTGCTGGAAGATGTTAGTTGATACGCTCCGATGTTCTTCAGTAAGATAG	9
Qy	600	attcccaac 607	
Db			
Db	8	ATTCCCAAC 1	

RESULT	15
AK017897	
LOCUS	AK017897 2219 bp mRNA linear HTC 19-JAN-2002
DEFINITION	Mus musculus adult male thymus cDNA, RIKEN full-length enriched library, clone:5830405C08:homolog to SYNTAXIN 11, full insert sequence.
ACCESSION	AK017897
VERSION	AK017897.1 GI:12857382
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (strain:C57BL/6J) adult male thymus cDNA to mRNA, clone_11b:RIKEN full-length enriched mouse cDNA library clone:5830405C08.
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (sites)
AUTHORS	Carninci,P. and Hayashizaki,Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2 (sites)
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	3 (sites)
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi.N., Ishi.Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913

RESULT 15
US-08-393-985-1
: Sequence 1, Application US/08393985
: Patent No. 5693476
: GENERAL INFORMATION:
: APPLICANT: Scheller, Richard H.
: TITLE OF INVENTION: Methods and Compositions for Modulation
: OF INVENTION: of Vesicular Release
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSER: Dehlinger & Associates
: STREET: 350 Cambridge Avenue, Suite 250

APPLICATION NUMBER: 135692/1992
FILING DATE: April 30, 1992
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 870
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-690-457-12

Query Match 9.6%; Score 124.8; DB 1; Length 870;

Best Local Similarity 60.7%; Pred. No. 6.3e-19;

Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 1 atccagccgagctggagatcatcggcgaaggaagtctcggcgaccagatcgagacatg 60
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445 ATCCAGCCGAGCTGGAGATCACTGGGAGGACCACCACCTGACGAGCTGGAAGAGATG 504
QY 61 ttcagcaggttaagtggagctgtttccgagaaacttgcggcgacgtgaaggcgcg 120
|||||
505 CTGGAGAGCGGAGCCGTCCTCATCTCGGATATTATATCATGATTCACAAATCACT 564
QY 121 cgggcccctcaacgagatcgagagccgaccgagctgctgcgctggagagccgc 180
|||||
565 AGGCAAGCTCATGATGATCGAGTCCCGCCACAAAGACATCATGAAGCTGGAGACCAGC 624
QY 181 atccgagctacacgagctcttcttcagatggcggtgctggagaaagcggcgac 240
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625 ATCCGAGAGCTGCAGAGATGTTATGATATGGCCATGTTTGTGAGACTCAGGGTGAA 684
QY 241 accctgaagctacgagctcaacgtacaaaagagcggtcgactacacggcgagcgaag 300
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685 ATGGTCAACAACATCGAGAGAAATGTGTGAACCTGTAGATTACGTGGAACATGCCAAG 744
QY 301 gcgcaggtgcggaagggcggtgcagtaaggagagaag 336
|||||
745 GAAGAGACGAAGAAAGCCATCAATACCAGAGCAAG 780
Db

RESULT 10

US-08-628-187-12

Sequence 12, Application US/08628187

Patent No. 5837239

GENERAL INFORMATION:

APPLICANT: BIOMATERIAL RESEARCH INSTITUTE CO., LTD.

TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE SUBSTANCE DESIGNATED

TITLE OF INVENTION: AS EPIMORPHIN, GENES ENCODING THE SAME, AND ANTIBODIES THEREO

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: 1, Taya-cho, Sakae-ku, Yokohama-shi, KANAGAWA, Japan

STREET: 1, Taya-cho

CITY: Yokohama-shi

COUNTRY: Japan

ZIP: 244

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/628,187

FILING DATE: April 5, 1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 294856/1991

FILING DATE: October 16, 1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 294857/1991

FILING DATE: October 16, 1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 122906/1992

FILING DATE: April 17, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 135692/1992
FILING DATE: April 30, 1992
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 870
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-628-187-12

Query Match 9.6%; Score 124.8; DB 2; Length 870;

Best Local Similarity 60.7%; Pred. No. 6.3e-19;

Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 1 atccagccgagctggagatcatcggcgaaggaagtctcggcgaccagatcgagacatg 60
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445 ATCCAGCCGAGCTGGAGATCACTGGGAGGACCACCACCTGACGAGCTGGAAGAGATG 504
QY 61 ttcagcaggttaagtggagctgtttccgagaaacttgcggcgacgtgaaggcgcg 120
|||||
505 CTGGAGAGCGGAGCCGTCCTCATCTCGGATATTATATCATGATTCACAAATCACT 564
QY 121 cgggcccctcaacgagatcgagagccgaccgagctgctgcgctggagagccgc 180
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565 AGGCAAGCTCATGATGATCGAGTCCCGCCACAAAGACATCATGAAGCTGGAGACCAGC 624
QY 181 atccgagctacacgagctcttcttcagatggcggtgctggagaaagcggcgac 240
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625 ATCCGAGAGCTGCAGAGATGTTATGATATGGCCATGTTTGTGAGACTCAGGGTGAA 684
QY 241 accctgaagctacgagctcaacgtacaaaagagcggtcgactacacggcgagcgaag 300
|||||
685 ATGGTCAACAACATCGAGAGAAATGTGTGAACCTGTAGATTACGTGGAACATGCCAAG 744
QY 301 gcgcaggtgcggaagggcggtgcagtaaggagagaag 336
|||||
745 GAAGAGACGAAGAAAGCCATCAATACCAGAGCAAG 780
Db

RESULT 11

US-08-690-457-15

Sequence 15, Application US/08690457

Patent No. 5726298

GENERAL INFORMATION:

APPLICANT: BIOMATERIAL RESEARCH INSTITUTE CO., LTD.

TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE SUBSTANCE

TITLE OF INVENTION: DESIGNATED AS EPIMORPHIN, GENES ENCODING THE SAME, AND ANTI

TITLE OF INVENTION: THERETO

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: 1, Taya-cho, Sakae-ku, Yokohama-shi, KANAGAWA,

STREET: 1, Taya-cho

CITY: Yokohama-shi

COUNTRY: Japan

ZIP: 244

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/690,457

FILING DATE: 16-AUG-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/078,309

FILING DATE: June 15, 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 294856/1991

QY 1 atccagcgcagctgagatcattggaagaaagctctcggcgccaccagatcaggagacatg 60
Db 445 ATCCAGCGCCAGCTGGAGATCATTGGAGGAGCACCACCTACGACGAGCTGGAAGAGATG 504
QY 61 ttcgagcagggttaagtggagcgtgttttcgagaaacttgcctgcccagcgtgaaggcgcg 120
Db 505 CTGGAGAGCGGGAAGCGCTCCTTCATCTCGGATATTATATCAGATTACAAATCACT 564
QY 121 cgggcgcctcaacgagatcagagacccgaccgcggaactgctgcgctggagagccgc 180
Db 565 AGCAAGCTCTCAATGAGATCGAGTCCCGCCACAAGACATCATGAAGCTGGAGACGAGC 624
QY 181 atccgcagctacacagctcttcttcagatgctgctggtggagaaagcagccgac 240
Db 625 ATCCGAGAGCTGCACGAGATGTTTCATGGATATGCGCATGTTTTCGAGACTCAGGGTGAA 684
QY 241 accctgaacgtctcagctcagctcaacgtacaaagacggtgcactacacggccagggccaa 300
Db 685 ATGGTCAACAACATCGAGAGAAATGTGTGAACCTCTGTAGATTACGTGGAACATGCCAAG 744
QY 301 ggcaggtgcggaagccgctgagtcagagagaag 336
Db 745 GAAGAGACGAAGAAGCCATCAATACCGAGCAAG 780

RESULT 6
US-08-628-187-14
; Sequence 14, Application US/08628187
; Patent No. 5837239
; GENERAL INFORMATION:
; APPLICANT: BIOMATERIAL RESEARCH INSTITUTE CO., LTD.
; TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE SUBSTANCE DESIGNATED
; TITLE OF INVENTION: AS EPIMORPHIN, GENES ENCODING THE SAME, AND ANTIBODIES THEREO
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: 1, Taya-cho, Sakae-ku, Yokohama-shi, KANAGAWA, Japan
; STREET: 1, Taya-cho
; CITY: Yokohama-shi
; COUNTRY: Japan
; ZIP: 244
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,187
; FILING DATE: April 5, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 294856/1991
; FILING DATE: October 16, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 294857/1991
; FILING DATE: October 16, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 122906/1992
; FILING DATE: April 17, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 135692/1992
; FILING DATE: April 30, 1992
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-628-187-14

Query Match 9.6%; Score 124.8; DB 2; Length 840;
Best Local Similarity 60.7%; Pred. No. 6.2e-19;

Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0:
QY 1 atccagcgcagctgagatcattggaagaaagctctcggcgccaccagatcaggagacatg 60
Db 445 ATCCAGCGCCAGCTGGAGATCATTGGAGGAGCACCACCTACGACGAGCTGGAAGAGATG 504
QY 61 ttcgagcagggttaagtggagcgtgttttcgagaaacttgcctgcccagcgtgaaggcgcg 120
Db 505 CTGGAGAGCGGGAAGCGCTCCTTCATCTCGGATATTATATCAGATTACAAATCACT 564
QY 121 cgggcgcctcaacgagatcagagacccgaccgcggaactgctgcgctggagagccgc 180
Db 565 AGCAAGCTCTCAATGAGATCGAGTCCCGCCACAAGACATCATGAAGCTGGAGACGAGC 624
QY 181 atccgcagctacacagctcttcttcagatgctgctggtggagaaagcagccgac 240
Db 625 ATCCGAGAGCTGCACGAGATGTTTCATGGATATGCGCATGTTTTCGAGACTCAGGGTGAA 684
QY 241 accctgaacgtctcagctcagctcaacgtacaaagacggtgcactacacggccagggccaa 300
Db 685 ATGGTCAACAACATCGAGAGAAATGTGTGAACCTCTGTAGATTACGTGGAACATGCCAAG 744
QY 301 ggcaggtgcggaagccgctgagtcagagagaag 336
Db 745 GAGAGACGAAGAAGCCATCAATACCGAGCAAG 780

RESULT 7
US-08-690-457-13
; Sequence 13, Application US/08690457
; Patent No. 5726298
; GENERAL INFORMATION:
; APPLICANT: BIOMATERIAL RESEARCH INSTITUTE CO., LTD.
; TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE SUBSTANCE
; TITLE OF INVENTION: DESIGNATED AS EPIMORPHIN, GENES ENCODING THE SAME, AND ANTI
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: 1, Taya-cho, Sakae-ku, Yokohama-shi, KANAGAWA,
; STREET: 1, Taya-cho
; CITY: Yokohama-shi
; COUNTRY: Japan
; ZIP: 244
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,457
; FILING DATE: 16-AUG-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/078,309
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 294856/1991
; FILING DATE: October 16, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 294857/1991
; FILING DATE: October 16, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 122906/1992
; FILING DATE: April 17, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 135692/1992
; FILING DATE: April 30, 1992
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 867
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

Qy	61	ttcagacagggtaagtgggacgtgttttccgagaacttctgcgcacactgctggcgacagtgaaggcgcg	120
Db	271	CTGGAGCGGGAAAGCGCTCCATCTTCATCTCGGATATTATATCAGATTCAAAATCACT	330
Qy	121	cggcgccctcaacgagatcagagagcgcgccacgcgaaactgctgcgctggagagccgc	180
Db	331	AGGCAAGCTCTCAATGAGATCGAGTCCCGCCACAAGACATCATGAAGCTGGAGACCAGC	390
Qy	181	atccgcgacgtacacgagctcttcttcagatggcgggtgctggtggagaagcaggccgac	240
Db	391	ATCCGAGAGCTGCACGAGATGTTTCATGGATATGGCCATGTTTCTCGAGACTCAGGGTGAA	450
Qy	241	acctgcaactcatcgagctccaagtacaaaagacagctgcactacaccggcgaggccaag	300
Db	451	ATGCTCAACAACATCGAGAGAAATGTGGTGAATCTGTAGATTACGTGGNACATGCCAAG	510
Qy	301	gcgcaggtgcggaaggccgtgcagctacgaggagaag	336
Db	511	GAAGAGACGGAAGAAAGCATCAAAATACCACAGCAAG	546

RESULTS

US-08-493-071-11
Sequence 11, Application US/08493071
Patent No. 6127149
GENERAL INFORMATION:
APPLICANT: Hirai, Yohei
APPLICANT: Koshida, Shogo
APPLICANT: Oka, Yumiko
TITLE OF INVENTION: MODIFIED EPIMORPHIN
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
STREET: 99 CANAL CENTER PLAZA, SUITE 300
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentrin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/493,071
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 715-107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-493-071-11

	Query Match	9.6%	Score 124.8	DB 3	Length 711	
	Best Local Similarity	60.7%	Pred. No. 5.8e-19			
	Matches 204	Conservative	0	Mismatches 132	Indels	Gaps 0
Qy	1	atccagcccgctggagatcatctggcgaagaagtctctggcgaccagatcgagagacatg	60			
	358	ATCCAGCCCGCAGCTGGAGATCACTGGGGAGGACCACCACTGACGAGCTGGGAAGAGATG	417			
Db						
Qy	61	ttcagcagcagggttaatggygcagctgtttcccgagaactctgtggccgcagctgaaggcgctg	120			
Qy						


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AA041593
ID AA041593 standard; cDNA; 867 BP.
XX
AC AA041593;
XX
DT 24-AUG-1993 (first entry)
DE Mouse epimorphin isoform A coding sequence.
XX
DE vascularisation; induction; epithelial tissue morphogenesis; ds.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 1..867
FT /tag= a
FT /product= epimorphin_isoform_A
XX
XX WO9308213-A.
XX
XX 29-APR-1993.
XX
XX 15-OCT-1992; 92WO-JP01340.
XX
XX 16-OCT-1991; 91JP-0294856.
XX
XX 16-OCT-1991; 91JP-0294857.
XX
XX 17-APR-1992; 92JP-0122906.
XX
XX 30-APR-1992; 92JP-0135692.
XX
XX (BIOM-) BIOMATERIAL RES INST CO LTD.
XX
XX Hirai Y, Takashina M, Takebe K;
XX
XX WPI; 1993-152423/18.
XX
XX P-PSDB; AAR36553.
XX
XX Novel active substance epimorphin, its gene and antibodies - for
XX diagnosing and treating epithelial diseases
XX
XX Claim 10; Page 56; 76pp; Japanese.
XX
XX This sequence encodes one of three isolated isoforms of mouse
XX epimorphin, a protein produced by mesenchymal cells and which
XX induces epithelial tissue morphogenesis. Modified forms of
XX epimorphin in which the C-terminal hydrophobic region is replaced
XX by a defective or non-hydrophobic peptide are also claimed.
XX See also AA041592 and AA041594.
XX
XX Sequence 867 BP; 261 A; 191 C; 246 G; 169 T; 0 other;

Query Match 9.6%; Score 124.8; DB 14; Length 867;
Best Local Similarity 60.7%; Pred. No. 4.3e-13;
Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 1 atccagccagctggagatcattggcgaagaagctctcgccgaccagatcgagacatg 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 445 atccagccagctggagatcattggcgaagaagctctcgccgaccagatcgagacatg 504

QY 61 ttccagcagggttaagtgggacgtgtttccgagaacttctgcccgcgtgaaggcgcg 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 505 ctggagagcgggaagccgtccattctctcgtgattatattatcagattcacaatact 564

QY 121 cgggcccctcaacgagatcgagagccgcaccgcggaactgtgcccctggagagccgc 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 565 aggaactctcaatgatgatgagtcgccgcacaaagacatcatgaagctggagaccagc 624

QY 181 atccgacatcacagagctctcttcagatgctgctgtgtgggaagaagcggccgac 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 625 atccgagagctgcacgagagtgctcatggatgtggccatgtttgtcgagactcagggtgaa 684

QY 241 accctgaactcagagctcaactcaaaagacgtgcactacacccgcccagggccaag 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 685 atgtcaacaacatcgagagaatgtgtgaactctgtgattacgtggaacatgccaaag 744
QY 301 gcgcaggtgcggaagccgtgcagtagcagagagaag 336
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 745 gaagagacgaagaagccatcaatacaccagagaag 780

RESULT 13
AAQ75248
ID AAQ75248 standard; cDNA; 867 BP.
XX
AC AAQ75248;
XX
XX 10-AUG-1995 (first entry)
XX
DE Mouse epimorphin isoform A gene.
XX
XX Probe; epimorphine; human; mouse; lambda-gt11; expression library;
XX monoclonal antibody; isoform; drug; congenital; acquired; E.coli;
XX epidermal abnormality; ds.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX variation 793..867
XX /tag= a
XX /note= "sequence variance in isoform A"
XX
XX JP06293800-A.
XX
XX 21-OCT-1994.
XX
XX 15-OCT-1992; 92JP-0301581.
XX
XX 15-OCT-1992; 92JP-0301581.
XX
XX (BIOM-) BIOMATERIAL KENKYUSHO KK.
XX
XX WPI; 1995-009638/02.
XX
XX P-PSDB; AAR66480.
XX
XX Human or murine epimorphine - useful for development of drugs to
XX treat congenital and acquired epidermal form abnormality
XX
XX Claim 10; Page 8; 41pp; Japanese.
XX
XX The sequence of the gene encoding mouse epimorphine isoform A. A DNA
XX fragment (AAQ75250) containing the mouse epimorphine gene (AAQ75247) was
XX isolated from a lambda-gt11 expression cDNA library screened with a
XX monoclonal antibody raised against mouse epimorphine. A probe
XX (AAQ75243) derived from the mouse gene sequence was used to isolate
XX isoforms of the mouse gene (AAQ75248-9) and the gene encoding human
XX epimorphine (AAQ75244) and isoforms (AAQ75245-6). The genes were cloned
XX into expression systems for the production of the protein in E.coli and
XX in animal cells. The epimorphine can be used in the development of drugs
XX to treat both congenital and acquired epidermal form abnormality.
XX
XX Sequence 867 BP; 261 A; 192 C; 245 G; 169 T; 0 other;

Query Match 9.6%; Score 124.8; DB 16; Length 867;
Best Local Similarity 60.7%; Pred. No. 4.3e-13;
Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 1 atccagccagctggagatcattggcgaagaagctctcgccgaccagatcgagacatg 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 445 atccagccagctggagatcattggcgaagaagctctcgccgaccagatcgagacatg 504

QY 61 ttccagcagggttaagtgggacgtgtttccgagaacttctgcccgcgtgaaggcgcg 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 505 ctggagagcgggaagccgtccattctctcgtgattatattatcagattcacaatact 564

QY 121 cgggcccctcaacgagatcgagagccgcaccgcggaactgtgcccctggagagccgc 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 505 aggaactctcaatgatgatgagtcgccgcacaaagacatcatgaagctggagaccagc 564

QY 181 atccgacatcacagagctctcttcagatgctgctgtgtgggaagaagcggccgac 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 505 atccgagagctgcacgagagtgctcatggatgtggccatgtttgtcgagactcagggtgaa 564

QY 241 accctgaactcagagctcaactcaaaagacgtgcactacacccgcccagggccaag 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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XX New polypeptides contain a first portion of 5-99 amino acids joined
CC to a second portion contg. at least a functional domain of
CC epimorphin. The first portion may be selected from the peptides
CC given in AAR92029 to AAR92036. The second portion may be full-length
CC epimorphin (see AAR92037 to AAR92042 for human and mouse epimorphins).
CC Fragments (123), (2M), (3M) and (23) of epimorphin given in AAT16083
CC to AAT16090 are used in the prodn. of modified epimorphins.
CC 123: N-terminus to right before C-terminal hydrophobic domain.
CC 2M: amino acid 30 to right before C-terminal hydrophobic domain.
CC 3M: amino acid 79 to right before C-terminal hydrophobic domain.
CC 23: amino acid 105 to right before C-terminal hydrophobic domain.
CC The modified epimorphins are useful for the development of diagnosis
CC and treatment of morphogenetic abnormalities of epithelial tissue or
CC novel remedies for wounds, eg burns, after surgery and for artificial
CC organs. They may also be used as components of cosmetics, hair
CC growth stimulators, etc.
XX
Sequence 798 BP; 251 A; 177 C; 230 G; 140 T; 0 other;

Query Match          9.6%; Score 124.8; DB 17; Length 798;
Best Local Similarity 60.7%; Pred. No. 4.3e-13;
Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 1 atccagcgcagctgagatcattggcgaaggagtcgtcgccgaccagatcgaggacatg 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 445 atccagcgcagctgagatcattggcgaaggagtcgtcgccgaccagatcgaggacatg 504

QY 61 ttcgagcagggttaagtggagcgtgttttcgagaaacttctggtcgccgacgtgaaggcgcg 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 505 ctggagagcgggaagcgtccattctctcggtatattatcagattcacaataact 564

QY 121 cgggcgcctcaacagatcgagaccgcaccgcgaactctgcgctgagagccgc 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 565 aggcagctctcaatgagatcgatccgcaccacaagacatcatgaagctggagaccagc 624

QY 181 atccgcgacgtacacagatcttcttcgagatggcgggtggtggaagcagccgcac 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 625 atccgagagctcagcagatgttcattgatatggccattgttcgagactcagggtgaa 684

QY 241 accctgaacgtcatcgagctcaacgtacaaaagacggtcgactacaccggccagccaag 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 685 atggtcaacaacatcgagagaaatgtgtgaactctgtagattacgtggaacatgccaa 744

QY 301 gcgcaggtgcggaagccgtgcagtcacgagagaag 336
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 745 gaagagacgaagaagccatcaataaccagagcaag 780

RESULT 9
AAT62414
ID AAT62414 standard; cDNA; 798 BP.
XX
XX AAT62414;
XX
XX 02-JUL-1997 (first entry)
XX
XX Mouse epimorphin coding sequence.
XX
XX Human; mouse; epimorphin; coiled-coil region; functional domain; tissue;
XX hydrophobic; deletion; truncation; regulation; morphogenesis; epithelium;
XX artificial organ; cosmetic; hair tonic; ds.
XX
XX Mus musculus.
XX
XX JP09065885-A.
XX
XX 11-MAR-1997.
XX
XX 29-MAR-1996; 96JP-0099684.
XX
XX 19-JUN-1995; 95JP-0175540.

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PR 31-MAR-1995; 95JP-0099980.
XX
XX (SUME ) SUMITOMO ELECTRIC IND CO.
XX
XX WPI; 1997-220419/20.
XX
XX Modified epimorphin and related DNA - useful e.g. for treatment of
XX tissues or in artificial organs, or as an ingredient in cosmetics
XX
XX Example 1; Page 14; 18pp; Japanese.
XX
XX The invention relates to novel human (AAW14257-9) or mouse (AAW14260-2)
XX epimorphin proteins with replacements, deletions or substitutions in the
XX amino acid sequence. The new epimorphin protein consists of: (a) an
XX N-terminal coiled-coil region; (b) a functional domain in the middle;
XX and (c) a C-terminal coiled-coil region. A hydrophobic region in the
XX C-terminal has been deleted and at least some amino acids have been
XX deleted from the terminals of coiled coil regions (a) and/or (c). This
XX sequence encodes the complete mouse epimorphin protein. Epimorphin is a
XX protein which regulates morphogenesis of epithelial tissues. It can be
XX used for treatment of tissues or used directly in artificial organs or
XX as an ingredient in cosmetics, hair tonic, etc.
XX
XX Sequence 798 BP; 251 A; 177 C; 230 G; 140 T; 0 other;
XX
XX
Query Match          9.6%; Score 124.8; DB 18; Length 798;
Best Local Similarity 60.7%; Pred. No. 4.3e-13;
Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 1 atccagcgcagctgagatcattggcgaaggagtcgtcgccgaccagatcgaggacatg 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 445 atccagcgcagctgagatcattggcgaaggagtcgtcgccgaccagatcgaggacatg 504

QY 61 ttcgagcagggttaagtggagcgtgttttcgagaaacttctggtcgccgacgtgaaggcgcg 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 505 ctggagagcgggaagcgtccattctctcggtatattatcagattcacaataact 564

QY 121 cgggcgcctcaacagatcgagaccgcaccgcgaactctgcgctgagagccgc 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 565 aggcagctctcaatgagatcgatccgcaccacaagacatcatgaagctggagaccagc 624

QY 181 atccgcgacgtacacagatcttcttcgagatggcgggtggtggaagcagccgcac 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 625 atccgagagctcagcagatgttcattgatatggccattgttcgagactcagggtgaa 684

QY 241 accctgaacgtcatcgagctcaacgtacaaaagacggtcgactacaccggccagccaag 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 685 atggtcaacaacatcgagagaaatgtgtgaactctgtagattacgtggaacatgccaa 744

QY 301 gcgcaggtgcggaagccgtgcagtcacgagagaag 336
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 745 gaagagacgaagaagccatcaataaccagagcaag 780

RESULT 10
AAQ41594
ID AAQ41594 standard; cDNA; 840 BP.
XX
XX AAQ41594;
XX
XX 24-AUG-1993 (first entry)
XX
XX Mouse epimorphin isoform B coding sequence.
XX
XX vascularisation; induction; epithelial tissue morphogenesis; ds.
XX
XX Mus musculus.
XX
XX OS
XX Key Location/Qualifiers
XX FH 1..840
XX CDS /*tag= a
XX FT /product= epimorphin_isoform_B
XX

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Db 451 atgtcaacaacatcgagagaaatgtgtgaactctgttagattacgtggaacatgccaaag 510
 Qy 301 gcgcaggtgcggaagccgtgcagtagcagagagaag 336
 Db 511 gaagagacgaagaagccatcaataaccagagcaag 546

RESULT 5
 AAT62412
 ID AAT62412 standard; cDNA; 564 BP.
 XX AC AAT62412;
 XX DT 02-JUL-1997 (first entry)
 XX DE Mouse epimorphin truncated variant. 3M coding sequence.
 XX KW Human; mouse; epimorphin; coiled-coil region; functional domain; tissue;
 KW hydrophobic; deletion; truncation; regulation; morphogenesis; epithelium;
 KW artificial organ; cosmetic; hair tonic; ds.
 XX SA Synthetic.
 XX OS JP09065885-A.
 XX PN 11-MAR-1997.
 XX PD 29-MAR-1996; 96JP-0099684.
 XX PF 19-JUN-1995; 95JP-0175540.
 XX PR 31-MAR-1995; 95JP-0099980.
 XX PA (SUME) SUMITOMO ELECTRIC IND CO.
 XX DR WPI; 1997-220419/20.
 XX DR P-PSDB; AAW14261.
 XX KW Modified epimorphin and related DNA - useful e.g. for treatment of
 PT tissues or in artificial organs, or as an ingredient in cosmetics
 XX Example 1; Page 13; 18pp; Japanese.

The invention relates to novel human (AAW14257-9) or mouse (AAW14260-2) epimorphin proteins with replacements, deletions or substitutions in the amino acid sequence. The new epimorphin protein consists of: (a) an N-terminal coiled-coil region; (b) a functional domain in the middle; and (c) a C-terminal coiled-coil region. A hydrophobic region in the C-terminal has been deleted and at least some amino acids have been deleted from the terminals of coiled coil regions (a) and/or (c). This sequence encodes the mouse epimorphin protein lacking the N-terminal 78 amino acids. Epimorphin is a protein which regulates morphogenesis of epithelial tissues. It can be used for treatment of tissues or used directly in artificial organs or as an ingredient in cosmetics, hair tonic, etc.

Sequence 564 BP; 181 A; 124 C; 162 G; 97 T; 0 other;
 Query Match 9.6%; Score 124.8; DB 18; Length 564;
 Best Local Similarity 60.7%; Pred. No. 4e-13;
 Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

Qy 1 atccagccagctggagatcatggcgaagaagtctcggcgaccagatcgaggacatg 60
 Db 211 atccagccagctggagatcatggcgaagaagtctcggcgaccagatcgaggacatg 270
 Qy 61 ttcagcagcaggtgaagtggagctgttttccgagaacttgcggcgacgtgaaggcgcg 120
 Db 271 ctgagagcgggagcgcgtccatctctcgtggtatattatcatcagattcaacaatcact 330
 Qy 121 cggcgccgcctcaacagatcgagagcgccacccgcaactgctgcgctggagagcgcg 180
 Db 331 aggcagctctcaatgagatcagctcccgcccaagaacatcatgaagctggagaccagc 390

Qy 181 atccgcagctacacgagctcttcttcagatgctggtggtggaagcagcgccgac 240
 Db 391 atccgcagctgcacgagatgttcattgatggtccatgttctgcgagactcaggggtgaa 450
 Qy 241 accctgaacgtcatcgtgagctcaacgtacaaaagacggtgcgactacacccgagcccaag 300
 Db 451 atggtcaacaacatcgagagaaatgtgtgaactctgtagattacgtggaacatgccaaag 510

Qy 301 gcgcaggtgcggaagccgtgcagtagcagagagaag 336
 Db 511 gaagagacgaagaagccatcaataaccagagcaag 546

RESULT 6
 AAT16086
 ID AAT16086 standard; cDNA; 711 BP.
 XX AC AAT16086;
 XX DT 30-MAY-1996 (first entry)
 XX DE Mouse epimorphin fragment (2M).
 XX KW Epimorphin; human; mouse; wound; burn; epithelial tissue;
 KW diagnosis; treatment; morphogenetic abnormality; cosmetic;
 KW hair growth stimulator; ds.
 XX OS Mus musculus.
 XX PN EP698666-A2.
 XX PD 28-FEB-1996.
 XX PF 20-JUN-1995; 95EP-0304270.
 XX PR 31-MAR-1995; 95JP-0099980.
 XX PR 21-JUN-1994; 94JP-0162874.
 XX PR 31-MAR-1995; 95JP-0099979.
 XX PA (SUME) SUMITOMO ELECTRIC IND CO.
 XX PT Hirai Y, Koshida S, Oka Y;
 XX WPI; 1996-118213/13.
 XX P-PSDB; AAR92046.

Novel polypeptide containing an epimorphin functional domain - has possible benefits in epithelial tissue treatments, e.g. burns and for artificial organs

Claim 27; Page 30; 62pp; English.

New polypeptides contain a first portion of 5-99 amino acids joined to a second portion contg. at least a functional domain of epimorphin. The first portion may be selected from the peptides given in AAR92029 to AAR92036. The second portion may be full-length epimorphin (see AAR92037 to AAR92042 for human and mouse epimorphins). Fragments (123), (2M), (3M) and (23) of epimorphin given in AAT16083 to AAT16090 are used in the prodn. of modified epimorphins.
 123: N-terminus to right before C-terminal hydrophobic domain.
 2M: amino acid 30 to right before C-terminal hydrophobic domain.
 3M: amino acid 79 to right before C-terminal hydrophobic domain.
 23: amino acid 105 to right before C-terminal hydrophobic domain.
 The modified epimorphins are useful for the development of diagnosis and treatment of morphogenetic abnormalities of epithelial tissue or novel remedies for wounds, eg burns, after surgery and for artificial organs. They may also be used as components of cosmetics, hair growth stimulators, etc.

Sequence 711 BP; 232 A; 155 C; 201 G; 123 T; 0 other;

PT during apoptosis and/or tumour suppression

PS Claim 1; Page 21; 24pp; French.

XX AA61474-87 represent tumour suppressor activated pathway gene cDNAs, designated TSAP9-TSAP22, respectively. The cellular expression of TSAP genes is induced during apoptosis and tumour suppression. The specification also describes a tumour suppressor inhibited pathway gene TSAP3. Medicaments comprising either vectors for cellular expression of the TSAP genes or TSAP3, proteins encoded by these genes, compounds that ensure cellular expression of these genes, or compounds that inhibit cellular expression of these genes are useful for treating cancer or as antiviral agents. Probes and primers derived from the genes and antigens or antibodies corresponding to TSAP or TSIP proteins are useful for diagnostic purposes, especially for identifying a predisposition to cancer and for monitoring cancer. Cells transformed with TSAP or TSIP genes can be used to screen for anticancer and antiviral agents.

Sequence 240 BP; 68 A; 54 C; 47 G; 71 T; 0 other;

Query Match 16.2%; Score 209.2; DB 21; Length 240;
Best Local Similarity 97.9%; Pred. No. 5.7e-28;
Matches 233; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

OY 685 atctgactgtaggtgaatgtctgagcgtcctcctaataaagactcaaggaggaagtc 744
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
OY 745 aattgggcatctgctaataagaatgaactcatgatggaacttcagttcattttgtc 804
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
OY 805 cctgaaattccctgttctgttccattttagcgaattggccttgggaaaccacgt 864
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
OY 121 cctgaaattccctgttctgttccattttagcgaattggccttgggaaaccacgt 180
OY 865 tcttcttccgattcttcacgttcacgttcacgttcacgttcacgttcacgttcacgt 922
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
OY 181 tcttcttccgattcttcacgttcacgttcacgttcacgttcacgttcacgttcacgt 237

RESULT 2

AA116088
ID AA116088 standard; cDNA; 486 BP.

XX NC AA116088;

XX DT 30-MAY-1996 (first entry)

XX DE Mouse epimorphin fragment (23).

KW Epimorphin; human; mouse; wound; burn; epithelial tissue;
KW diagnosis; treatment; morphogenetic abnormality; cosmetic;
KW hair growth stimulator; ds.

XX OS Mus musculus.

XX PN EP98666-A2.

XX PD 28-FEB-1996.

XX PF 20-JUN-1995; 95EP-0304270.

XX PR 31-MAR-1995; 95JP-0099980.

XX PR 21-JUN-1994; 94JP-0162874.

XX PR 31-JUN-1995; 95JP-0099979.

XX PA (SUME) SUMITOMO ELECTRIC IND CO.

XX PI Hiral Y, Koshida S, Oka Y;

XX

DR WPI: 1996-118213/13.
DR P-FSDB; AAR92048.

XX Novel polypeptide containing an epimorphin functional domain - has possible benefits in epithelial tissue treatments, e.g. burns and for artificial organs

XX Claim 27; Page 32; 62pp; English.

XX New polypeptides contain a first portion of 5-99 amino acids joined to a second portion contg. at least a functional domain of epimorphin. The first portion may be selected from the peptides given in AAR92029 to AAR92036. The second portion may be full-length epimorphin (see AAR92037 to AAR92042 for human and mouse epimorphins). Fragments (123), (2M), (3M) and (23) of epimorphin given in AAR16083 to AAR16090 are used in the prodn. of modified epimorphins.

CC 123: N-terminus to right before C-terminal hydrophobic domain.

CC 2M: amino acid 30 to right before C-terminal hydrophobic domain.

CC 3M: amino acid 79 to right before C-terminal hydrophobic domain.

CC 23: amino acid 105 to right before C-terminal hydrophobic domain.

CC The modified epimorphins are useful for the development of diagnosis and treatment of morphogenetic abnormalities of epithelial tissue or novel remedies for wounds, eg burns, after surgery and for artificial organs. They may also be used as components of cosmetics, hair growth stimulators, etc.

XX Sequence 486 BP; 152 A; 110 C; 139 G; 85 T; 0 other;

Query Match 9.6%; Score 124.8; DB 17; Length 486;
Best Local Similarity 60.7%; Pred. No. 3.9e-13;
Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

OY 1 atccagccagctgagatcatcagggaaggagctcggcgaccagatcaggagacatg 60
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
OY 133 atccagccagctgagatcactggaggagaccactgacgagctggaagagatg 192
OY 61 ttcgagcagggtaagtgggaaggtgtttccgagaacttgcggcgacgtgaaggcg 120
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
OY 193 ctggagagcgggaagccgtccatcttcctcgatattatcagattcacaatcact 252
OY 121 cgggcccctccacgagatcagagcgcaccgcgaactcgtcgcctggagagccgc 180
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
OY 253 aggcagctcctcaatgagatcagtgctccgcccacaaagacatcatgaagtggagaccag 312
OY 181 atccgcagctacacgagctcttcttcgagatgcgggtgctgtggaagagcgcgcac 240
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
OY 313 atccgcagcgtcgcagcagatgctcagtgatggtccatgttctgcgagactcagggtgaa 372
OY 241 accctgaacgtcctcagctcaacgtacaaaagacggtcgcactacacccgcccagccaaag 300
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
OY 373 atggtcaacaacatcgcagagaaatgtgtgaactctgtagattacgtggaacatgccaaag 432
OY 301 gcgcaggtgcgggaagccgctgcagtcacgagagagaag 336
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
OY 433 gaagagcagaaagccatcaataaccagagcaag 468

RESULT 3

AA162413
ID AA162413 standard; cDNA; 486 BP.

XX AC AA162413;

XX DT 02-JUL-1997 (first entry)

XX Mouse epimorphin truncated variant 23 coding sequence.

DE Human; mouse; epimorphin; coiled-coil region; functional domain; tissue;
KW hydrophobic; deletion; truncation; regulation; morphogenesis; epithelium;
KW artificial organ; cosmetic; hair tonic; ds.

XX Synthetic.

OS

Qy 301 ggcaggtgcggaagccgtgcagtcagagagaag 336
 Db 433 GAAGAGACGAAGAAGCCATCAATATACCAAGCAAG 468

RESULT 12
 AR111443
 LOCUS AR111443 564 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 12 from patent US 6127149.
 ACCESSION AR111443
 VERSION AR111443.1 GI:12828291
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 564)
 AUTHORS Hirai,Y., Koshida,S. and Oka,Y.
 TITLE Modified epimorphin
 JRNAL Patent: US 6127149-A 12 OCT-2000;
 FEATURES Location/Qualifiers
 source 1..564
 BASE COUNT 181 a 124 c 162 g 97 t
 ORIGIN

Query Match 9.6%; Score 124.8; DB 6; Length 564;
 Best Local Similarity 60.7%; Pred. No. 4e-10;
 Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

Qy 1 atccagcgcagctggagatcatggcaaggaagctctcggcgccagcatcgagacatg 60
 Db 211 ATCCAGCGCCAGCTGGAGATCACTGGGAGGACCACCATGAGCAGCGCTGGAAGATG 270

Qy 61 ttcagcagggtaagtggagcgtgtttccagagaacttctggtggagagcgtgaaggcgcg 120
 Db 271 CTGAGAGCGGGAAGCCGTCATCTTCATCTCGGATATTATATCAGATTCAAAATCACT 330

Qy 121 cggcgccctcaacagatcgagagccgacccagcaactgctgcctgagagccgc 180
 Db 331 AGGCAAGCTCTCAATGATCGATGCTCCGCCCAAGACATCATGAAGCTGGAGACCAGC 390

Qy 181 atccgcagctacacgagctcttcttcagatggcggctggtggagagcagcgcgcac 240
 Db 391 ATCCGAGAGCTGCAGAGATCTTCATGATATGCCATGTTTGTGCGAGACTCAGGGTGA 450

Qy 241 accctgaactcagagctcaacgatacaaaagacggtcgactacacgcccagggccaag 300
 Db 451 ATGCTCAACAACATCGAGAGAAATGTGTGAACCTCTGTAGATTACGTGGAACATGCCAAG 510

Qy 301 ggcaggtgcggaagccgtgcagtcagagagaag 336
 Db 511 GAAGAGACGAAGAAGCCATCAATATACCAAGCAAG 546

RESULT 13
 E12727
 LOCUS E12727 564 bp DNA linear PAT 24-JUN-1998
 DEFINITION DNA encoding mouse Epimorphin-derived peptide.
 ACCESSION E12727
 VERSION E12727.1 GI:3251559
 KEYWORDS JP 1997065885-A/6.
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 564)
 AUTHORS Koshida,S., Oka,Y. and Hirai,Y.
 TITLE TAILORED DERIVATIVE OF EPIMORPHIN
 JOURNAL Patent: JP 1997065885-A 6 11-MAR-1997;
 COMMENT SUMITOMO ELECTRIC IND LTD
 OS None
 OC Artificial sequences.

PN JP 1997065885-A/6
 PD 11-MAR-1997
 PF 29-MAR-1996 JP 1996099684
 PR 31-MAR-1995 JP 95P 99880, 19-JUN-1995 JP 95P 175540 PI
 KOSHIDA SHOGO, OKA YUMIKO, HIRAI YOHEI
 PC C12N15/09, C07H21/04, C07K7/06, C07K14/485, PC
 C12P21/02//A61K38/00,
 PC (C12P21/02,C12R1:19);
 CC strandedness: Double;
 CC topology: Linear;
 FH key Location/Qualifiers
 FH source 1..564
 FT /organism='Artificial sequences' FT
 mat_peptide 1..561
 FT /product='Epimorphin fragment designated FT
 (3M)'/notes='fragment (3M) is derived 79-265 aa of
 mouse Epimorphin'.
 FT Location/Qualifiers
 source 1..564
 /organism='unidentified'
 /db_xref='taxon:32644'
 BASE COUNT 181 a 124 c 162 g 97 t
 ORIGIN

Query Match 9.6%; Score 124.8; DB 6; Length 564;
 Best Local Similarity 60.7%; Pred. No. 4e-10;
 Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

Qy 1 atccagcgcagctggagatcatggcaaggaagctctcggcgccagcatcgagacatg 60
 Db 211 ATCCAGCGCCAGCTGGAGATCACTGGGAGGACCACCATGAGCAGCGCTGGAAGATG 270

Qy 61 ttcagcagggtaagtggagcgtgtttccagagaacttctggtggagagcgtgaaggcgcg 120
 Db 271 CTGAGAGCGGGAAGCCGTCATCTTCATCTCGGATATTATATCAGATTCAAAATCACT 330

Qy 121 cggcgccctcaacagatcgagagccgacccagcaactgctgcctgagagccgc 180
 Db 331 AGGCAAGCTCTCAATGATCGATGCTCCGCCCAAGACATCATGAAGCTGGAGACCAGC 390

Qy 181 atccgcagctacacgagctcttcttcagatggcggctggtggagagcagcgcgcac 240
 Db 391 ATCCGAGAGCTGCAGAGATGTTTCATGATATGCCATGTTTGTGCGAGACTCAGGGTGA 450

Qy 241 accctgaactcagagctcaacgatacaaaagacggtcgactacacgcccagggccaag 300
 Db 451 ATGCTCAACAACATCGAGAGAAATGTGTGAACCTCTGTAGATTACGTGGAACATGCCAAG 510

Qy 301 ggcaggtgcggaagccgtgcagtcagagagaag 336
 Db 511 GAAGAGACGAAGAAGCCATCAATATACCAAGCAAG 546

RESULT 14
 AR111442
 LOCUS AR111442 711 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 11 from patent US 6127149.
 ACCESSION AR111442
 VERSION AR111442.1 GI:12828290
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 711)
 AUTHORS Hirai,Y., Koshida,S. and Oka,Y.
 TITLE Modified epimorphin
 JOURNAL Patent: US 6127149-A 11 OCT-2000;
 FEATURES Location/Qualifiers
 source 1..711

polyA_site 229 68 a 54 c 47 g 71 t

BASE COUNT

ORIGIN

Query Match 16.2%; Score 209.2; DB 9; Length 240;
Best Local Similarity 97.9%; Pred. No. 2.5e-23;
Matches 233; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 685 atctgactgaagggaatgtctgagcgtgctccttaataaagactcaaggaggagtc 744
|||||
Db 2 ATCTGACTGAGGGGAATGCTGAGGCTGCTCCTTAATAAGACTCAAGGAGGAGTC 61
|||||

QY 745 aattgggcatctgctaataagaactcatgatggaacttcagttcatttactttgtc 804
|||||
Db 62 AATTGGGCATCTGCTAATAGATGACTCATGATGGAATCTCAGTTCAATTACTTTGT- 120
|||||

QY 805 cctgaataatcctcgttctgttccatttggagcaaatggccttgggaaacacacgt 864
|||||
Db 121 CCTGAAATTCCTGGTCTGTTCTCCATTTGAGCGAAATGGCTTGGGAAAAACCCACGT 180
|||||

QY 865 tcttcttccgattctcattcgcgttctacgctgatgcaattcctcccaaatataga 922
|||||
Db 181 TCTTCTTCCGATCTTCATCGGCTAC-GCTATGCAATTCTCTCCCAAAAAA 237
|||||

RESULT 8

LOCUS G32623 156 bp DNA linear STS 24-SEP-1999

DEFINITION A009K37 Human Homo sapiens STS genomic, sequence tagged site.

ACCESSION G32623

VERSION G32623.1 GI:5923144

KEYWORDS STS.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 156)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Adams, M.D.

TITLE Human STS sequences

JOURNAL Unpublished

COMMENT

Contact: Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Email: mdadams@tigr.org
Primer A: CATACATGTCATATGTAATCAA
Primer B: CGGCTATATTTGGGTATTATT
STS size: 156
PCR Profile:
Denaturation: 96C 5min
Anneal: 54C 30sec
Extend: 72C 30sec
Denature: 95C 30sec
FinalExtend: 72C 5min
Cycles: 30

Protocol:
GenomicDNA: 25 ng
Primer: 0.43 uM each
dNTPs: 230 uM each
Amplify: 0.5 units
TagStart Ab: 0.5 units
Total Volume: 10 ul

Buffer:
Tris-HCl pH8.8: 100 mM
KCl: 500 mM
MgCl2: 20 mM
Triton X-100: 1%
Concentration: 10X

Prepared with primer pairs derived from THCL20341: GenBank
Accession Numbers- R65594, R33852, T25062, L70341.

Location/Qualifiers
1..156
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human"
1..156
1..23
primer_bind
primer_bind
complement(134..156) 48 t
BASE COUNT 65 a 22 c 21 g 48 t
ORIGIN

Query Match 10.5%; Score 135.6; DB 11; Length 156;
Best Local Similarity 94.0%; Pred. No. 6.9e-12;
Matches 141; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1017 tatatttggtattattttccaaacatttttaagcactgaatatcgaaacactcaa 1076
|||||
Db 150 TATTTTGGGTATTATTTTCCCAACATTTTAAAGCACTGAATATGCAACAGCACTCAA 91
|||||

QY 1077 attgaagtacgtcattgttgcgtatttttcgctgataaaaaattatttaacattata 1136
|||||
Db 90 ATTGAAGTATCATGTCATGTTTGTGTTATTTTCGCTGATAAAAAATTATTTAACATTATA 31
|||||

QY 1137 ttttacttgattacatgcacatgtatg 1166
|||||
Db 30 TTTTACTTGTATCATATGACATGTATG 1
|||||

RESULT 9

LOCUS RATSNTX2B 825 bp mRNA linear ROD 26-OCT-1993

DEFINITION Rattus norvegicus syntaxin 2', mRNA, complete cds.

ACCESSION L20888

VERSION L20888.1 GI:349314

KEYWORDS syntaxin 2; vesicular transport receptor.

SOURCE Rattus norvegicus (library: lambda Zap II) cDNA to mRNA.

ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 825)
Bennett, M.K., Garcia-Ararras, J.E., Elferink, L.A., Peterson, K.,
Fleming, A.M., Hazuka, C.D. and Scheller, R.H.
The syntaxin family of vesicular transport receptors
Cell 74 (5), 863-873 (1993)

AUTHORS Cell 74 (5), 863-873 (1993)

TITLE

JOURNAL

MEDLINE 93386759

FEATURES
Location/Qualifiers
1..825
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/tissue_lib="lambda Zap II"
1..825
/note="syntaxin 2', differs from syntaxin 2 and 2' only at
the carboxyl terminal end in the transmembrane region"
/codon_start=1
/product="syntaxin 2'"
/protein_id="AA03048.1"
/db_xref="GI:349315"

CDS

BASE COUNT 252 a 187 c 242 g 144 t
ORIGIN

Query Match 9.7%; Score 125.4; DB 10; Length 825;
Best Local Similarity 58.4%; Pred. No. 3.4e-10;
Matches 219; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY 1 atccagccagctggagatcatgggcaaggagtctcggcgaccagatcgaggacatg 60

AUTHORS Amson, R.B.
 TITLE Direct Submission
 JOURNAL Submitted (22-OCT-1998) Amson R.B., Tumor Suppression, CEPH Human Polymorphism Study Center, 27 rue Juliet Dodu Paris, 75010, FRANCE
 FEATURES Location/Qualifiers
 source 1..1296
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /cell_line="K562"
 /clone="TSAP21 extended"
 polyA_signal 723..728
 polyA_site 1262
 BASE COUNT 370 a 305 c 282 g 339 t
 ORIGIN
 Query Match 99.2%; Score 1284; DB 9; Length 1296;
 Best Local Similarity 99.9%; Pred. No. 1.2e-190;
 Matches 1295; Conservative 0; Mismatches 0; Indels 1; Gaps 1
 C 1 attcagcgccagctggagatcatgtggcaaggaagtctcgggcgaccagatcagaggacatg 60
 |||||
 Db 1 ATCCAGGCCAGCTGGAGATCATGGCAAGGAAGTCTCGGCGCACCATCGAGGACATG 60
 |||||
 QY 61 ttccagcagggttaagtgggacgtgtttcccgagaactgtctgcccagacdtgaaggcg-cgc 119
 |||||
 Db 61 TTCGAGCAGGGTAAGTGGGACGTGTTTCCGAGAACTTGCTGGCGACGCTGAAGGCCCG 120
 |||||
 QY 120 gcggcgccctcaacgagatcgagagcgcgcacgcgcaactgtcgcctggagagccg 179
 |||||
 Db 121 CGGGCGCCCTCAACGAGATCGAGAGCGGCCACCGCAACTGCTGCGCTTGGAGGCCG 180
 |||||
 QY 180 catccgcagctcacagagctcttcttcagatggcgtgctggtggaagcagcgccga 239
 |||||
 Db 181 CATCGCGACGTACACGAGCTCTCTTCGAGATGGCGGTGCTGTGTGGAGAAAGCAGGCCCA 240
 |||||
 QY 240 caccctgaacgtcatcgagctcaacgtaacaaagacggtcgcatacacccgcgcaggccaa 299
 |||||
 Db 241 CACCTGAACGTCTATCGAGCTCAACGTCACAAAGACGGTCGACTACACCGCGCCAGGCCAA 300
 |||||
 QY 300 ggccaggtgcggaagccgtgcagtcagagagaagaacccctccggaccctctgctg 359
 |||||
 Db 301 GGCGCAGGTGCGAAGGCCGTGCAGTCAGGAGAAGAACCCCTCGCGGACCTCTGTCTG 360
 |||||
 QY 360 ctctgctgctccctgcctcaagtagcagcgccgcgcgcgcgcacccctccagccatcccgag 419
 |||||
 Db 361 CTCTGCTGTCCCTGCCTCAAGTACAGCGCGCCCGCGGCCCGCCACCGCTCCAGAC 420
 |||||
 QY 420 catggagcgctgggaagcagctcaccaaagccgggagctcgcctcagggagttgc 479
 |||||
 Db 421 CATGGAGCGCCTGGGAAGGAGCTCACCAAAGCCGGAGCTGTGCCCTCGAGGGAGTTGC 480
 |||||
 QY 480 cccaaccttccggaaactcagctcttagaaaagaaacccaggttcaagaattcaaac 539
 |||||
 Db 481 CCCAACCTTTCCGGAACTCAGTCTTTAGAAAGAAACCCAGGTTCAAGAAATTGCAAA 540
 |||||
 QY 540 cagcctgtgctggaaagatggttagttgatccctccgatgatcttctcagtaaaagatag 599
 |||||
 Db 541 CAGCCTGTGCTTGAAAGATGTTAGTTGATACCGTCCGATCATCTTCAGTAAGATAG 600
 |||||
 QY 600 attcccaaaagtgtgcaatgtcatatataagacaccttgcaactttaccgtcttgacag 659
 |||||
 Db 601 ATTCCCAAAAGTTGTGCAATGTCTATTATGACACCTTGGCACTCTTACCGTCTTGACAG 660
 |||||
 QY 660 aagccaagtaaggaaactgaattgtatctgactgtagggtgaattctctgagggcctgcctc 719
 |||||
 Db 661 AAGCCAAGTAGGAACCTGAAGTTGATCTGACTGTGAGGTGAATGTCTGAGGCCCTGCCCTC 720
 |||||
 QY 720 ctaataagactcaaggaggaagtcgaattgggcacatctcgtctaataagaatgaactcatgatg 779
 |||||
 Db 721 CTATAAAGACTCAAGGAGGAAGTCGAATTTGGGCATCTGCTAATAGAATGAACATCATGATG 780
 |||||
 QY 780 gaaacttcagttcatttacttctgtccctgaaaaattccctgggtctctgttccattttgagcg 839
 |||||

